Listing of Claims:

The listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1-23 (cancelled)

Claim 24 (currently amended) A method of analyzing a subset of nucleic acids within a nucleic acid population, comprising:

(a) providing a driver population of nucleic acids and a tester population of nucleic acids;

(b) denaturing said driver population of nucleic acids and said tester population of nucleic acids;

(c) annealing said driver population to said tester population to produce a single-stranded subset of nucleic acids and a double-stranded subset of nucleic acids;

(d) immobilizing said driver population of nucleic acids to produce an unimmobilized single-stranded tester subset of nucleic acids, an immobilized double-stranded tester-driver subset of nucleic acids and an immobilized single-stranded driver subset of nucleic acids;

(e) separating said unimmobilized single-stranded tester subset of nucleic acids from said immobilized double-stranded tester-driver subset of nucleic acids and said immobilized single-stranded driver subset of nucleic acids;

(f) dissociating said immobilized double-stranded tester-driver subset of nucleic acids to produce a subset of complementary tester nucleic acids and a subset of immobilized complementary driver nucleic acids;

(g) separating said subset of complementary tester nucleic acids from said subset of immobilized complementary driver nucleic acids;

(h) hybridizing said subset of complementary tester nucleic acids to probes on a nucleic acid probe array, wherein a first subset of said probes is designed to be perfectly complementary to said subset of complementary nucleic acids; and

(i) determining which of said probes on said array hybridize to said subset of complementary tester nucleic acids, thereby analyzing said subset of complementary tester nucleic acids.

Claim 25 (original) The method of claim 24, wherein said driver population is a population of genomic DNA fragments, and said tester population is mRNA or nucleic acids derived therefrom.

Claim 26 (original) The method of claim 24, wherein said driver population is a population of genomic DNA fragments from a first source, and said tester population is genomic DNA from a second source.

Claim 27 (original) The method of claim 26, wherein said tester population is from a genome of a first individual, and said driver population is from a genome of a different individual of a same species as said first individual.

Claim 28 (original) The method of claim 26, wherein said tester population is from a genome of a first individual, and said driver population is from a genome of an individual of a different species than said first individual.

Claim 29 (original) The method of claim 24, wherein either said driver population or said tester population or both said driver and said tester populations is a PCR amplification product.

Claim 30 (original) The method of claim 24, wherein said driver population is from a plurality of noncontiguous regions of a genome of a species.

Claim 31 (original) The method of claim 30, wherein said driver population is from at least ten noncontiguous regions.

Claim 32 (original) The method of claim 24, wherein said driver population is mRNA or nucleic acids derived therefrom, and said tester population is genomic DNA.

Claim 33 (original) The method of claim 24, wherein said driver population is mRNA or nucleic acids derived therefrom from a first source, and said tester population is mRNA or nucleic acids derived therefrom from a second source.

Claim 34 (original) The method of claim 33, wherein said first source is from a tissue of a first species, and said second source is from a same tissue of a different species.

Claim 35 (original) The method of claim 33, wherein said first source is from a first tissue of a first species, and said second source is from a different tissue of said first species.

Claim 36 (original) The method of claim 24, wherein said immobilizing step is performed before said annealing step.

Claim 37 (original) The method of claim 24, wherein said immobilizing step is performed before said first denaturing step.

Claim 38 (original) The method of claim 24, wherein said driver population of nucleic acids each bear a tag by which said driver population can be immobilized to a binding moiety with affinity for said tag.

Claim 39 (original) The method of claim 38, wherein said tag is biotin, and said binding moiety is avidin or streptavidin.

Claim 40 (original) The method of claim 39, wherein said first separating step is performed by immobilizing said driver population of nucleic acids and tester population of nucleic acids hybridized to said driver population via said tags on said driver population.

Claim 41 (new) The method of claim 24, wherein said driver population is a PCR amplification product and said tester population is genomic DNA.

Claim 42 (new) The method of claim 41, wherein said genomic DNA is from more than one individual.

Claim 43 (new) The method of claim 41, wherein said PCR amplification product is a long-range PCR amplification product.

Claim 44 (new) The method of claim 41, wherein said tester population is subject to at least one amplification reaction.

Claim 45 (new) The method of claim 44, wherein said amplification reaction is performed prior to step (a) or after said separating step.

Claim 46 (new) A method of analyzing a subset of nucleic acids within a nucleic acid population, comprising:

(a) providing a driver population of nucleic acids and a tester population of nucleic acids, wherein said tester population of nucleic acids comprises genomic DNA;

(b) denaturing said driver population of nucleic acids and said tester population of nucleic acids;

(c) annealing said driver population to said tester population to produce a single-stranded subset of nucleic acids and a double-stranded subset of nucleic acids;

(d) immobilizing said driver population of nucleic acids to produce an unimmobilized single-stranded tester subset of nucleic acids, an immobilized double-stranded tester-driver subset of nucleic acids and an immobilized single-stranded driver subset of nucleic acids;

(e) separating said unimmobilized single-stranded tester subset of nucleic acids from said immobilized double-stranded tester-driver subset of nucleic acids and said immobilized single-stranded driver subset of nucleic acids;

(f) dissociating said immobilized double-stranded tester-driver subset of nucleic acids to produce a subset of complementary tester nucleic acids and a subset of immobilized complementary driver nucleic acids;

(g) separating said subset of complementary tester nucleic acids from said subset of immobilized complementary driver nucleic acids;

(h) hybridizing said subset of complementary tester nucleic acids to probes on a nucleic acid probe array, wherein a first subset of said probes is designed to be perfectly complementary to said subset of complementary nucleic acids; and

(i) determining which of said probes on said array hybridize to said subset of complementary tester nucleic acids, thereby analyzing said subset of complementary tester nucleic acids.

Claim 47 (new) The method of claim 46, wherein said driver population is a population of genomic DNA fragments, and said tester population is mRNA or nucleic acids derived therefrom.

Claim 48 (new) The method of claim 46, wherein said driver population is a population of genomic DNA fragments from a first source, and said tester population is genomic DNA from a second source.

Claim 49 (new) The method of claim 48, wherein said tester population is from a genome of a first individual, and said driver population is from a genome of a different individual of a same species as said first individual.

Claim 50 (new) The method of claim 48, wherein said tester population is from a genome of a first individual, and said driver population is from a genome of an individual of a different species than said first individual.

Claim 51 (new) The method of claim 46, wherein either said driver population or said tester population or both said driver and said tester populations is a PCR amplification product.

Claim 52 (new) The method of claim 46, wherein said driver population is from a plurality of noncontiguous regions of a genome of a species.

Claim 53 (new) The method of claim 52, wherein said driver population is from at least ten noncontiguous regions.

Claim 54 (new) The method of claim 46, wherein said driver population is mRNA or nucleic acids derived therefrom, and said tester population is genomic DNA.

Claim 55 (new) The method of claim 46, wherein said driver population is mRNA or nucleic acids derived therefrom from a first source, and said tester population is mRNA or nucleic acids derived therefrom from a second source.

Claim 56 (new) The method of claim 55, wherein said first source is from a tissue of a first species, and said second source is from a same tissue of a different species.

Claim 57 (new) The method of claim 55, wherein said first source is from a first tissue of a first species, and said second source is from a different tissue of said first species.

Claim 58 (new) The method of claim 46, wherein said immobilizing step is performed before said annealing step.

Claim 59 (new) The method of claim 46, wherein said immobilizing step is performed before said first denaturing step.

Claim 60 (new) The method of claim 46, wherein said driver population of nucleic acids each bear a tag by which said driver population can be immobilized to a binding moiety with affinity for said tag.

Claim 61 (new) The method of claim 60, wherein said tag is biotin, and said binding moiety is avidin or streptavidin.

Claim 62 (new) The method of claim 61, wherein said first separating step is performed by immobilizing said driver population of nucleic acids and tester population of nucleic acids hybridized to said driver population via said tags on said driver population.